SEQUENCE LISTING

<110> MOCKEL, BETTINA

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HANS, STEFAN

KREUTZER, CAROLINE

HERMANN, THOMAS

PFEFFERLE, WALTER

BINDER, MICHAEL

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<151> 2001-02-16

<150> DE 10162386.0

<151> 2001-12-19

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tccgaaataa ggatggttc atg cca act att cag cag ctg gtc cgt aag ggc       532
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cgc cac gat aag tcc gcc aag gtg gct acc gcg gca ctg aag ggt tcc       580
Arg His Asp Lys Ser Ala Lys Val Ala Thr Ala Ala Leu Lys Gly Ser
              15                  20                  25
```

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cct cag cgt cgt ggc gta tgc acc cgt gtg tac acc acc acc cct aag       628
Pro Gln Arg Arg Gly Val Cys Thr Arg Val Tyr Thr Thr Thr Pro Lys
          30                  35                  40
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aag cct aac tct gct ctt cgt aag gtc gct cgt gtg cgc ctt acc tcc       676
Lys Pro Asn Ser Ala Leu Arg Lys Val Ala Arg Val Arg Leu Thr Ser
      45                  50                  55
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ggc atc gag gtt tcc gct tac atc cct ggt gag ggc cac aac ctg cag       724
Gly Ile Glu Val Ser Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln
60                  65                  70                  75
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gag cac tcc atg gtg ctc gtt cgc ggt ggt cgt gtt aag gac ctc cca       772
Glu His Ser Met Val Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro
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Glu His Ser Met Val Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro
                    80                  85                  90

ggt gtc cgt tac aag atc gtc cgt ggc gca ctg gat acc cag ggt gtt    820
Gly Val Arg Tyr Lys Ile Val Arg Gly Ala Leu Asp Thr Gln Gly Val
             95                  100                 105

aag gac cgc aag cag gct cgt tcc ccg cta cgg cgc gaa gag ggg ata    868
Lys Asp Arg Lys Gln Ala Arg Ser Pro Leu Arg Arg Glu Glu Gly Ile
            110                 115                 120

att aaa aat gcg taaatcagca gctcctaagc gtccagtagt tcaggaccct        920
Ile Lys Asn Ala
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gtatacaagt ccgagctcgt tacccagctc gtaaacaaga tcctcatcgg tggcaagaag    980

tccaccgcag agcgcatcgt ctacggtgca ctcgagatct gccgtgagaa gaccggcacc   1040

gatccagtag gaaccctcga gaaggctctc ggcaacgtgc gtccagacct cgaagttcgt   1100

tccggccgtg ttggtggcgc tacctaccag gtgccagtgg atgttcgccc agagcgcgca   1160

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aacaagagaa ttatccgtag gtgacaaact ttttaatact tgggtatctg tcatggatac   1640

cccggtaata aataagtgaa ttaccgtaac caacaagttg gggtaccact gtggcacaag   1700

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            20   25   30

Val Cys Thr Arg Val Tyr Thr Thr Thr Pro Lys Lys Pro Asn Ser Ala
        35   40   45

Leu Arg Lys Val Ala Arg Val Arg Leu Thr Ser Gly Ile Glu Val Ser
    50   55   60

Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln Glu His Ser Met Val
65   70   75   80

Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr Lys
                85   90   95

Ile Val Arg Gly Ala Leu Asp Thr Gln Gly Val Lys Asp Arg Lys Gln
            100   105   110

Ala Arg Ser Pro Leu Arg Arg Glu Glu Gly Ile Ile Lys Asn Ala
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<213>   Corynebacterium glutamicum

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tcggttaagg tcagtggcga gcttctttgc tggttcgttt ccttgaggaa cagtcatggg   180

aaccattcta caagggatt tggtgttttc tgcggctagc tgataatgtg aacggctgag   240

tcccactctt gtagttggga attgacggca cctcgcactc aagcgcggta tcgcccctgg   300

ttttccggga cgcggtggcg catgtttgca tttgatgagg ttgtccgtga catgtttggt   360

cgggccccaa aaagagcccc cttttttgcg tgtctggaca ctttttcaaa tccttcgcca   420

tcgacaagct cagccttcgt gttcgtcccc cgggcgtcac gtcagcagtt aaagaacaac   480

tccgaaataa ggatggttc atg cca act att cag cag ctg gtc cgt aag ggc   532
                      Met Pro Thr Ile Gln Gln Leu Val Arg Lys Gly
                       1   Pro 5   10

cgc cac gat aag tcc gcc aag gtg gct acc gcg gca ctg aag ggt tcc   580
Arg His Asp Lys Ser Ala Lys Val Ala Thr Ala Ala Leu Lys Gly Ser
            15   20   25

cct cag cgt cgt ggc gta tgc acc cgt gtg tac acc acc acc cct agg   628
Pro Gln Arg Arg Gly Val Cys Thr Arg Val Tyr Thr Thr Thr Pro Arg
        30   35   40

aag cct aac tct gct ctt cgt aag gtc gct cgt gtg cgc ctt acc tcc   676
Lys Pro Asn Ser Ala Leu Arg Lys Val Ala Arg Val Arg Leu Thr Ser
    45   50   55

ggc atc gag gtt tcc gct tac atc cct ggt gag ggc cac aac ctg cag   724
Gly Ile Glu Val Ser Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln
60   65   70   75

gag cac tcc atg gtg ctc gtt cgc ggt ggt cgt gtt aag gac ctc cca   772
Glu His Ser Met Val Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro
                80   85   90

ggt gtc cgt tac aag atc gtc cgt ggc gca ctg gat acc cag ggt gtt   820
Gly Val Arg Tyr Lys Ile Val Arg Gly Ala Leu Asp Thr Gln Gly Val
            95   100   105

aag gac cgc aag cag gct cgt tcc ccg cta cgg cgc gaa gag ggg ata   868

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Lys Asp Arg Lys Gln Ala Arg Ser Pro Leu Arg Arg Glu Glu Gly Ile
        110                 115                 120

att aaa aat gcg taaatcagca gctcctaagc gtccagtagt tcaggaccct           920
Ile Lys Asn Ala
    125

gtatacaagt ccgagctcgt tacccagctc gtaaacaaga tcctcatcgg tggcaagaag     980

tccaccgcag agcgcatcgt ctacggtgca ctcgagatct gccgtgagaa gaccggcacc    1040

gatccagtag gaaccctcga gaaggctctc ggcaacgtgc gtccagacct cgaagttcgt    1100

tcccgccgtg ttggtggcgc tacctaccag gtgccagtgg atgttcgccc agagcgcgca    1160

aacaccctcg cactgcgttg gttggtaacc ttcacccgtc agcgtcgtga aacaccatg     1220

atcgagcgtc ttgcaaacga acttctggat gcagccaacg gccttggcgc ttccgtgaag    1280

cgtcggcaag acacccacaa gatggcagag gccaaccgcg ccttcgctca ctaccgctgg    1340

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aacaggagaa ttatccgtag gtgacaaact ttttaatact tgggtatctg tcatggatac    1640

cccggtaata aataagtgaa ttaccgtaac caacaagttg gggtaccact gtggcacaag    1700

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<211>    127

<212>    PRT

<213>    Corynebacterium glutamicum


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1               5                   10                  15
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Ala Lys Val Ala Thr Ala Ala Leu Lys Gly Ser Pro Gln Arg Arg Gly
        20   25   30

Val Cys Thr Arg Val Tyr Thr Thr Thr Pro Arg Lys Pro Asn Ser Ala
        35   40   45

Leu Arg Lys Val Ala Arg Val Arg Leu Thr Ser Gly Ile Glu Val Ser
    50   55   60

Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln Glu His Ser Met Val
65   70   75   80

Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr Lys
                85   90   95

Ile Val Arg Gly Ala Leu Asp Thr Gln Gly Val Lys Asp Arg Lys Gln
            100   105   110

Ala Arg Ser Pro Leu Arg Arg Glu Glu Gly Ile Ile Lys Asn Ala
        115   120   125

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<211> 5099

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<213> Corynebacterium glutamicum

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<222> (702)..(4196)

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tcgacgcctc cctcgacgat gcagctgtct ctaagctggt tgcacaggcc gaaagcatcc        180

ctgatggaga tgtgagcaaa atcgcaaata ccgtaggtat tgtgatcggt gcggtattgg        240

ctctcgtggg cctggccggg tgttttgggg cgtttgggaa gaaacgtcga gaagcttaac        300

ctgctgttca aatagatttt ccctgtttcg aattgcggaa accccgggtt tgtttgctag        360

ggtgcctcgt agaaggggtc aagaagattt ctgggaaacg cgcccgtgcg gttggttgct        420

aatagcacgc ggagcaccag atgaaaaatc tcccctttac tttcgcgcgc gattggtata        480

ctctgagtcg ttgcgttgga attcgtgact cttttcgtt cctgtagcgc caagaccttg         540

atcaaggtgg tttaaaaaaa ccgatttgac aaggtcattc agtgctatct ggagtcgttc        600

agggggatcg ggttcctcag cagaccaatt gctcaaaaat accagcggtg ttgatctgca        660

cttatggcc ttgaccagcc aggtgcaatt acccgcgtga g gtg ctg gaa gga ccc        716
                                             Val Leu Glu Gly Pro
                                             1                   5

atc ttg gca gtc tcc cgc cag acc aag tca gtc gtc gat att ccc ggt        764
Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val Val Asp Ile Pro Gly
              10              15                  20

gca ccg cag cgt tat tct ttc gcg aag gtg tcc gca ccc att gag gtg        812
Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser Ala Pro Ile Glu Val
          25              30                  35

ccc ggg cta cta gat ctt caa ctg gat tct tac tcc tgg ctg att ggt        860
Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr Ser Trp Leu Ile Gly
          40              45                  50

acg cct gag tgg cgt gct cgt cag aag gaa gaa ttc ggc gag gga gcc        908
Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu Phe Gly Glu Gly Ala
55              60                  65

cgc gta acc agc ggc ctt gag aac att ctc gag gag ctc tcc cca atc        956
Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu Glu Leu Ser Pro Ile
70              75                  80                  85

cag gat tac tct gga aac atg tcc ctg agc ctt tcg gag cca cgc ttc       1004
Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu Ser Glu Pro Arg Phe
                  90              95                  100

gaa gac gtc aag aac acc att gac gag gcg aaa gaa aag gac atc aac       1052
Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys Glu Lys Asp Ile Asn
          105                 110                 115
```

```
tac gcg gcg cca ctg tat gtg acc gcg gag ttc gtc aac aac acc acc        1100
Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe Val Asn Asn Thr Thr
        120                 125                 130

ggt gaa atc aag tct cag act gtc ttc atc ggc gat ttc cca atg atg        1148
Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly Asp Phe Pro Met Met
        135                 140                 145

acg gac aag gga acg ttc atc atc aac gga acc gaa cgc gtt gtg gtc        1196
Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr Glu Arg Val Val Val
150                 155                 160                 165

agc cag ctc gtc cgc tcc ccg ggc gtg tac ttt gac cag acc atc gat        1244
Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe Asp Gln Thr Ile Asp
                170                 175                 180

aag tca act gag cgt cca ctg cac gcc gtg aag gtt att cct tcc cgt        1292
Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys Val Ile Pro Ser Arg
                    185                 190                 195

ggt gct tgg ctt gag ttt gac gtc gat aag cgc gat tcg gtt ggt gtt        1340
Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg Asp Ser Val Gly Val
                    200                 205                 210

cgt att gac cgc aag cgt cgc cag cca gtc acc gta ctg ctg aag gct        1388
Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr Val Leu Leu Lys Ala
        215                 220                 225

ctt ggc tgg acc act gag cag atc acc gag cgt ttc ggt ttc tct gaa        1436
Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg Phe Gly Phe Ser Glu
230                 235                 240                 245

atc atg atg tcc acc ctc gag tcc gat ggt gta gca aac acc gat gag        1484
Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val Ala Asn Thr Asp Glu
                250                 255                 260

gca ttg ctg gag atc tac cgc aag cag cgt cca ggc gag cag cct acc        1532
Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro Gly Glu Gln Pro Thr
                265                 270                 275

cgc gac ctt gcg cag tcc ctc ctg gac aac agc ttc ttc cgt gca aag        1580
Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser Phe Phe Arg Ala Lys
        280                 285                 290

cgc tac gac ctg gct cgc gtt ggt cgt tac aag atc aac cgc aag ctc        1628
Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys Ile Asn Arg Lys Leu
        295                 300                 305

ggc ctt ggt ggc gac cac gat ggt ttg atg act ctt act gaa gag gac        1676
Gly Leu Gly Gly Asp His Asp Gly Leu Met Thr Leu Thr Glu Glu Asp
310                 315                 320                 325
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atc gca acc acc atc gag tac ctg gtg cgt ctg cac gca ggt gag cgc      1724
Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu His Ala Gly Glu Arg
            330                 335                 340

gtc atg act tct cca aat ggt gaa gag atc cca gtc gag acc gat gac      1772
Val Met Thr Ser Pro Asn Gly Glu Glu Ile Pro Val Glu Thr Asp Asp
            345                 350                 355

atc gac cac ttt ggt aac cgt cgt ctg cgt acc gtt ggc gaa ctg atc      1820
Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr Val Gly Glu Leu Ile
            360                 365                 370

cag aac cag gtc cgt gtc ggc ctg tcc cgc atg gag cgc gtt gtt cgt      1868
Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met Glu Arg Val Val Arg
            375                 380                 385

gag cgt atg acc acc cag gat gcg gag tcc att act cct act tcc ttg      1916
Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile Thr Pro Thr Ser Leu
390                     395                 400                 405

atc aac gtt cgt cct gtc tct gca gct atc cgt gag ttc ttc gga act      1964
Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg Glu Phe Phe Gly Thr
                410                 415                 420

tcc cag ctg tct cag ttc atg gtc cag aac aac tcc ctg tct ggt ttg      2012
Ser Gln Leu Ser Gln Phe Met Val Gln Asn Asn Ser Leu Ser Gly Leu
                425                 430                 435

act cac aag cgt cgt ctg tcg gct ctg ggc ccg ggt ggt ctg tcc cgt      2060
Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro Gly Gly Leu Ser Arg
                440                 445                 450

gag cgc gcc ggc atc gag gtt cga gac gtt cac cca tct cac tac ggc      2108
Glu Arg Ala Gly Ile Glu Val Arg Asp Val His Pro Ser His Tyr Gly
        455                 460                 465

cgt atg tgc cca att gag act ccg gaa ggt cca aac att ggc ctg atc      2156
Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro Asn Ile Gly Leu Ile
470                 475                 480                 485

ggt tcc ttg gct tcc tat gct cga gtg aac cca ttc ggt ttc att gag      2204
Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro Phe Gly Phe Ile Glu
                490                 495                 500

acc cca tac cgt cgc atc atc gac ggc aag ctg acc gac cag att gac      2252
Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu Thr Asp Gln Ile Asp
            505                 510                 515

tac ctt acc gct gat gag gaa gac cgc ttc gtt gtt gcg cag gca aac      2300
Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val Val Ala Gln Ala Asn
            520                 525                 530
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acg cac tac gac gaa gag ggc aac atc acc gat gag acc gtc act gtt     2348
Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp Glu Thr Val Thr Val
    535                 540                 545

cgt ctg aag gac ggc gac atc gcc atg gtt ggc cgc aac gcg gtt gat     2396
Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly Arg Asn Ala Val Asp
550                 555                 560                 565

tac atg gac gtt tcc cct cgt cag atg gtt tct gtt ggt acc gcg atg     2444
Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser Val Gly Thr Ala Met
                570                 575                 580

att cca ttc ctg gag cac gac gat gct aac cgt gca ctg atg ggc gcg     2492
Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ala
                585                 590                 595

aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc     2540
Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe
                600                 605                 610

gtg ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg     2588
Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu
    615                 620                 625

gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc     2636
Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe
630                 635                 640                 645

atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt     2684
Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg
                650                 655                 660

aag ttc cag cgc acc aac cag ggc acc agc tac aac cag aag cct ttg     2732
Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr Asn Gln Lys Pro Leu
                665                 670                 675

gtt aac ttg ggc gag cgc gtt gaa gct ggc cag gtt att gct gat ggt     2780
Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln Val Ile Ala Asp Gly
    680                 685                 690

cca ggt acc ttc aat ggt gaa atg tcc ctt ggc cgt aac ctt ctg gtt     2828
Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly Arg Asn Leu Leu Val
    695                 700                 705

gcg ttc atg cct tgg gaa ggc cac aac tac gag gat gcg atc atc ctc     2876
Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu Asp Ala Ile Ile Leu
710                 715                 720                 725

aac cag aac atc gtt gag cag gac atc ttg acc tcg atc cac atc gag     2924
Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr Ser Ile His Ile Glu
                730                 735                 740
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gag cac gag atc gat gcc cgc gac act aag ctt ggc gcc gaa gaa atc          2972
Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu Gly Ala Glu Glu Ile
            745             750                 755

acc cgc gac atc cct aat gtg tct gaa gaa gtc ctc aag gac ctc gac          3020
Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val Leu Lys Asp Leu Asp
        760             765                 770

gac cgc ggt att gtc cgc atc ggt gct gat gtt cgt gac ggc gac atc          3068
Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val Arg Asp Gly Asp Ile
    775             780             785

ctg gtc ggt aag gtc acc cct aag ggc gag acc gag ctc acc ccg gaa          3116
Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr Glu Leu Thr Pro Glu
790             795             800             805

gag cgc ttg ctg cgc gca atc ttc ggt gag aag gcc cgc gaa gtt cgc          3164
Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys Ala Arg Glu Val Arg
                810             815             820

gat acc tcc atg aag gtg cct cac ggt gag acc ggc aag gtc atc ggc          3212
Asp Thr Ser Met Lys Val Pro His Gly Glu Thr Gly Lys Val Ile Gly
                825             830             835

gtg cgt cac ttc tcc cgc gag gac gac gac gat ctg gct cct ggc gtc          3260
Val Arg His Phe Ser Arg Glu Asp Asp Asp Asp Leu Ala Pro Gly Val
        840             845             850

aac gag atg atc cgt atc tac gtt gct cag aag cgt aag atc cag gac          3308
Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys Arg Lys Ile Gln Asp
    855             860             865

ggc gat aag ctc gct ggc cgc cac ggt aac aag ggt gtt gtc ggt aaa          3356
Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys Gly Val Val Gly Lys
870             875             880             885

att ttg cct cag gaa gat atg cca ttc ctt cca gac ggc act cct gtt          3404
Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro Asp Gly Thr Pro Val
                890             895             900

gac atc atc ttg aac acc cac ggt gtt cca cgt cgt atg aac att ggt          3452
Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg Arg Met Asn Ile Gly
            905             910             915

cag gtt ctt gag acc cac ctt ggc tgg ctg gca tct gct ggt tgg tcc          3500
Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala Ser Ala Gly Trp Ser
        920             925             930

gtg gat cct gaa gat cct gag aac gct gag ctc gtc aag act ctg cct          3548
Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr Leu Pro
    935             940             945
```

```
gca gac ctc ctc gag gtt cct gct ggt tcc ttg act gca act cct gtg        3596
Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr Pro Val
950                 955                 960                 965

ttc gac ggt gcg tca aac gaa gag ctc gca ggc ctg ctc gct aat tca        3644
Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly Leu Leu Ala Asn Ser
                    970                 975                 980

cgt cca aac cgc gac ggc gac gtc atg gtt aac gcg gat ggt aaa gca        3692
Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly Lys Ala
                985                 990                 995

acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg gtt           3737
Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro Val
            1000                1005                1010

tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac           3782
Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp
            1015                1020                1025

gag aag atc cac gca cgt tcc act ggt cct tac tcc atg att acc           3827
Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr
            1030                1035                1040

cag cag cca ctg ggt ggt aaa gca cag ttc ggt gga cag cgt ttc           3872
Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe
            1045                1050                1055

ggc gaa atg gag gtg tgg gca atg cag gca tac ggc gct gcc tac           3917
Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr
            1060                1065                1070

aca ctt cag gag ctg ctg acc atc aag tct gat gac gtg gtt ggc           3962
Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp Asp Val Val Gly
            1075                1080                1085

cgt gtc aag gtc tac gaa gca att gtg aag ggc gag aac atc ccg           4007
Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly Glu Asn Ile Pro
            1090                1095                1100

gat cca ggt att cct gag tcc ttc aag gtt ctc ctc aag gag ctc           4052
Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu Leu Lys Glu Leu
            1105                1110                1115

cag tcc ttg tgc ctg aac gtg gag gtt ctc tcc gca gac ggc act           4097
Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser Ala Asp Gly Thr
            1120                1125                1130

cca atg gag ctc gcg ggt gac gac gac gac ttc gat cag gca ggc           4142
Pro Met Glu Leu Ala Gly Asp Asp Asp Asp Phe Asp Gln Ala Gly
            1135                1140                1145
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gcc tca ctt  ggc atc aac ctg tcc  cgt gac gag cgt tcc  gac gcc      4187
Ala Ser Leu  Gly Ile Asn Leu Ser  Arg Asp Glu Arg Ser  Asp Ala
        1150                 1155                 1160

gac acc gca  tagcagatca gaaaacaacc gctagaaatc aagccataca            4236
Asp Thr Ala
        1165

tccccccggac attgaagaga tgttctgggg ggaaagggag ttttacgtgc tcgacgtaaa   4296

cgtcttcgat gagctccgca tcggcctggc caccgccgac gacatccgcc gttggtccaa   4356

gggtgaggtc aagaagccgg agaccatcaa ctaccgaacc ctcaagcctg agaaggacgg   4416

tctgttctgc gagcgtatct tcggtccaac tcgcgactgg gagtgcgcct gcggtaagta   4476

caagcgtgtc cgctacaagg gcatcatctg tgaacgctgt ggcgttgagg tcaccaagtc   4536

caaggtgcgc cgtgagcgca tgggacacat tgagctcgct gcaccagtaa cccacatttg   4596

gtacttcaag ggcgttccat cacgcctcgg ctaccttttg gaccttgctc caaaggacct   4656

ggacctcatc atctacttcg gtgcgaacat catcaccagc gtggacgaag aggctcgcca   4716

cagcgaccag accactcttg aggcagaaat gcttctggag aagaaggacg ttgaggcaga   4776

cgcagagtct gacattgctg agcgtgctga aaagctcgaa gaggatcttg ctgaacttga   4836

ggcagctggc gctaaggccg acgctcgccg caaggttcag gctgctgccg ataaggaaat   4896

gcagcacatc cgtgagcgtg cacagcgcga atcgatcgt ctcgatgagg tctggcagac    4956

cttcatcaag cttgctccaa agcagatgat ccgcgatgag aagctctacg atgaactgat   5016

cgaccgctac gaggattact tcaccggtgg tatgggtgca gagtccattg aggctttgat   5076

                                                                     5099
ccagaacttc gaccttgatg ctg
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<210> 6

<211> 1165

<212> PRT

<213> Corynebacterium glutamicum

<400> 6

Val Leu Glu Gly Pro Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val

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Val Asp Ile Pro Gly Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser
              20   25   30

Ala Pro Ile Glu Val Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr
              35   40   45

Ser Trp Leu Ile Gly Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu
      50   55   60

Phe Gly Glu Gly Ala Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu
65   70   75   80

Glu Leu Ser Pro Ile Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu
                    85   90   95

Ser Glu Pro Arg Phe Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys
                    100   105   110

Glu Lys Asp Ile Asn Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe
              115   120   125

Val Asn Asn Thr Thr Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly
      130   135   140

Asp Phe Pro Met Met Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr
145   150   155   160

Glu Arg Val Val Val Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe
                    165   170   175

Asp Gln Thr Ile Asp Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys
              180   185   190

Val Ile Pro Ser Arg Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg
              195   200   205

Asp Ser Val Gly Val Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr

Val Leu Leu Lys Ala Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg
225   230   235   240

Phe Gly Phe Ser Glu Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val
         245   250   255

Ala Asn Thr Asp Glu Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro
         260   265   270

Gly Glu Gln Pro Thr Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser
         275   280   285

Phe Phe Arg Ala Lys Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys
         290   295   300

Ile Asn Arg Lys Leu Gly Leu Gly Gly Asp His Asp Gly Leu Met Thr
305   310   315   320

Leu Thr Glu Glu Asp Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu
         325   330   335

His Ala Gly Glu Arg Val Met Thr Ser Pro Asn Gly Glu Glu Ile Pro
         340   345   350

Val Glu Thr Asp Asp Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr
         355   360   365

Val Gly Glu Leu Ile Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met
         370   375   380

Glu Arg Val Val Arg Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile
385   390   395   400

Thr Pro Thr Ser Leu Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg
         405   410   415

Glu Phe Phe Gly Thr Ser Gln Leu Ser Gln Phe Met Val Gln Asn Asn

Ser Leu Ser Gly Leu Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro
      435   440   445

Gly Gly Leu Ser Arg Glu Arg Ala Gly Ile Glu Val Arg Asp Val His
    450   455   460

Pro Ser His Tyr Gly Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro
465   470   475   480

Asn Ile Gly Leu Ile Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro
          485   490   495

Phe Gly Phe Ile Glu Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu
        500   505   510

Thr Asp Gln Ile Asp Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val
     515   520   525

Val Ala Gln Ala Asn Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp
    530   535   540

Glu Thr Val Thr Val Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly
545   550   555   560

Arg Asn Ala Val Asp Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser
          565   570   575

Val Gly Thr Ala Met Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg
        580   585   590

Ala Leu Met Gly Ala Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg
     595   600   605

Ala Glu Ala Pro Phe Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr
    610   615   620

Asp Ala Gly Asp Leu Val Ile Thr Pro Val Ala Gly Val Val Glu Asn

Val Ser Ala Asp Phe Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu
                645   650   655

Thr Tyr Leu Leu Arg Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr
            660   665   670

Asn Gln Lys Pro Leu Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln
        675   680   685

Val Ile Ala Asp Gly Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly
    690   695   700

Arg Asn Leu Leu Val Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu
705   710   715   720

Asp Ala Ile Ile Leu Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr
                725   730   735

Ser Ile His Ile Glu Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu
            740   745   750

Gly Ala Glu Glu Ile Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val
    755   760   765

Leu Lys Asp Leu Asp Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val
    770   775   780

Arg Asp Gly Asp Ile Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr
785   790   795   800

Glu Leu Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys
            805   810   815

Ala Arg Glu Val Arg Asp Thr Ser Met Lys Val Pro His Gly Glu Thr
            820   825   830

Gly Lys Val Ile Gly Val Arg His Phe Ser Arg Glu Asp Asp Asp Asp

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Leu Ala Pro Gly Val Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys
 850 855 860

Arg Lys Ile Gln Asp Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys
865 870 875 880

Gly Val Val Gly Lys Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro
 885 890 895

Asp Gly Thr Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg
 900 905 910

Arg Met Asn Ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala
 915 920 925

Ser Ala Gly Trp Ser Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu
 930 935 940

Val Lys Thr Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu
945 950 955 960

Thr Ala Thr Pro Val Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly
 965 970 975

Leu Leu Ala Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn
 980 985 990

Ala Asp Gly Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr
 995 1000 1005

Pro Tyr Pro Val Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His
 1010 1015 1020

His Leu Val Asp Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr
 1025 1030 1035

Ser Met Ile Thr Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly

```
        1040                        1045                        1050

Gly Gln  Arg Phe Gly Glu Met  Glu Val Trp Ala Met  Gln Ala Tyr
         1055                        1060                        1065

Gly Ala  Ala Tyr Thr Leu Gln  Glu Leu Leu Thr Ile  Lys Ser Asp
         1070                        1075                        1080

Asp Val  Val Gly Arg Val Lys  Val Tyr Glu Ala Ile  Val Lys Gly
         1085                        1090                        1095

Glu Asn  Ile Pro Asp Pro Gly  Ile Pro Glu Ser Phe  Lys Val Leu
         1100                        1105                        1110

Leu Lys  Glu Leu Gln Ser Leu  Cys Leu Asn Val Glu  Val Leu Ser
         1115                        1120                        1125

Ala Asp  Gly Thr Pro Met Glu  Leu Ala Gly Asp Asp  Asp Asp Phe
         1130                        1135                        1140

Asp Gln  Ala Gly Ala Ser Leu  Gly Ile Asn Leu Ser  Arg Asp Glu
         1145                        1150                        1155

Arg Ser  Asp Ala Asp Thr Ala
         1160                        1165


<210>   7

<211>   151

<212>   DNA

<213>   Corynebacterium glutamicum


<400>   7
ggttgccggt aatcctgttg cggacaatat ttacaggatc tgacacattg ggcatcgctg      60

ggggagtggt ctcgtaggcc gccggcgcat aggaggcgcc gggaaattgc tgaccaagca     120

gagtgtaggg attgtcgttc acatcagaga t                                    151
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<210> 8

<211> 1926

<212> DNA

<213> Corynebacterium glutamicum

<400> 8

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ggttgccggt aatcctgttg cggacaatat ttacaggatc tgacacattg ggcatcgctg    60

ggggagtggt ctcgtaggcc gccggcgcat aggaggcgcc gggaaattgc tgaccaagca   120

gagtgtaggg attgtcgttc acatcagaga tcagctctac aagagtgtct aagtggcggg   180

catcccatgc tttggaggag cgatcttcaa attcctccaa agtgagttga cctcgggaaa   240

cagctgcaga aagttcatcc acgacttggt ttcggttaag gtcagtggcg agcttctttg   300

ctggttcgtt ccttgagga acagtcatgg gaaccattct aacaagggat ttggtgtttt   360

ctgcggctag ctgataatgt gaacggctga gtcccactct tgtagttggg aattgacggc   420

acctcgcact caagcgcggt atcgccctg gttttccggg acgcggtggc gcatgtttgc   480

atttgatgag gttgtccgtg acatgtttgg tcgggcccca aaaagagccc cttttttgc   540

gtgtctggac acttttcaa atccttcgcc atcgacaagc tcagccttcg tgttcgtccc   600

ccgggcgtca cgtcagcagt aaagaacaa ctccgaaata aggatggttc atgccaacta   660

ttcagcagct ggtccgtaag ggccgccacg ataagtccgc caaggtggct accgcggcac   720

tgaagggttc ccctcagcgt cgtggcgtat gcaccgtgt gtacaccacc acccctaaga   780

agcctaactc tgctcttcgt aaggtcgctc gtgtgcgcct acctccggc atcgaggttt   840

ccgcttacat ccctggtgag ggccacaacc tgcaggagca ctccatggtg ctcgttcgcg   900

gtggtcgtgt taaggacctc ccaggtgtcc gttacaagat cgtccgtggc gcactggata   960

cccagggtgt taaggaccgc aagcaggctc gttccccgct acggcgcgaa gaggggataa  1020

ttaaaaatgc gtaaatcagc agctcctaag cgtccagtag ttcaggaccc tgtatacaag  1080

tccgagctcg ttacccagct cgtaaacaag atcctcatcg gtggcaagaa gtccaccgca  1140

gagcgcatcg tctacggtgc actcgagatc tgccgtgaga agaccggcac cgatccagta  1200

ggaaccctcg agaaggctct cggcaacgtg cgtccagacc tcgaagttcg ttcccgccgt  1260
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gttggtggcg ctacctacca ggtgccagtg gatgttcgcc cagagcgcgc aaacaccctc      1320

gcactgcgtt ggttggtaac cttcacccgt cagcgtcgtg agaacaccat gatcgagcgt      1380

cttgcaaacg aacttctgga tgcagccaac ggccttggcg cttccgtgaa gcgtcgcgaa      1440

gacacccaca agatggcaga ggccaaccgc gccttcgctc actaccgctg gtagtactgc      1500

caagacatga aagcccaatc acctttaaga tcaacgcctg ccggcgccct tcacatttga      1560

ataagctggc agcctgcgtt tcttcaaggc gactgggctt ttagtctcat taatgcagtt      1620

caccgctgta agatagctaa atagaaacac tgtttcggca gtgtgttact aaaaaatcca      1680

tgtcacttgc ctcgagcgtg ctgcttgaat cgcaagttag tggcaaaatg taacaagaga      1740

attatccgta ggtgacaaac tttttaatac ttgggtatct gtcatggata ccccggtaat      1800

aaataagtga attaccgtaa ccaacaagtt ggggtaccac tgtggcacaa gaagtgctta      1860

aggatctaaa caaggtccgc aacatcggca tcatggcgca catcgatgct ggtaagacca      1920

cgatcca                                                                1926
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<220> 9

<211> 1594

<212> DNA

<213> Artificial sequence

<220>

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<220>

<221> allele

<222> (659)..(1039)

<223> rpsL-1545 allele

<220>

<221> mutation

<222> (86)..(86)

<223> a to g

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catcgctggg ggagtggtct cgtaggccgc cggcgcatag gaggcgccgg gaaattgctg     120

accaagcaga gtgtagggat tgtcgttcac atcagagatc agctctacaa gagtgtctaa     180

gtggcgggca ttccatgctt tggaggagcg atcttcaaat cctccaaag tgagttgacc      240

tcgggaaaca gctgcagaaa gttcatccac gacttggttt cggttaaggt cagtggcgag     300

cttctttgct ggttcgtttc cttgaggaac agtcatggga accattctaa caagggattt     360

ggtgttttct gcggctagct gataatgtga acggctgagt cccactcttg tagttgggaa     420

ttgacggcac ctcgcactca agcgcggtat cgcccctggt tttccgggac gcggtggcgc     480

atgtttgcat ttgatgaggt tgtccgtgac atgtttggtc gggcccccaaa aagagccccc    540

tttcttgcgt gtctggacac tttttcaaat ccttcgccat cgacaagctc agccttcgtg     600

ttcgtcccccc gggcgtcacg tcagcagtta aagaacaact ccgaaataag gatggttcat    660

gccaactatt cagcagctgg tccgtaaggg ccgccacgat aagtccgcca aggtggctac     720

cgcggcactg aagggttccc ctcagcgtcg tggcgtatgc acccgtgtgt acaccaccac     780

ccctaggaag cctaactctg ctcttcgtaa ggtcgctcgt gtgcgcctta cctccggcat     840

cgaggtttcc gcttacatcc ctggtgaggg ccacaacctg caggagcact ccatggtgct     900

cgttcgcggt ggtcgtgtta aggacctccc aggtgtccgt tacaagatcg tccgtggcgc     960

actggatacc cagggtgtta aggaccgcaa gcaggctcgt tccccgctac ggcgcgaaga    1020

ggggataatt aaaaatgcgt aaatcagcag ctcctaagcg tccagtagtt caggaccctg    1080

tatacaagtc cgagctcgtt acccagctcg taaacaagat cctcatcggt ggcaagaagt    1140

ccaccgcaga gcgcatcgtc tacggtgcac tcgagatctg ccgtgagaag accggcaccg    1200

atccagtagg aaccctcgag aaggctctcg caacgtgcg tccagacctc gaagttcgtt     1260

cccgccgtgt tggtggcgct acctaccagg tgccagtgga tgttcgccca gagcgcgcaa    1320

acaccctcgc actgcgttgg ttggtaacct tcacccgtca gcgtcgtgag aacaccatga    1380
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tcgagcgtct  tgcaaacgaa  cttctggatg  cagccaacgg  ccttggcgct  tccgtgaagc       1440

gtcgcgaaga  cacccacaag  atggcagagg  ccaaccgcgc  cttcgctcac  taccgctggt       1500

agtactgcca  agacatgaaa  gcccaatcac  ctttaagatc  aacgcctgcc  ggcgcccttc       1560

acatttgaat  aagctggcag  cctgcgtcta  gatc                                     1594
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<210> 10

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic DNA

<400> 10
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cagctctaca  agagtgtcta                                                          20
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<210> 11

<211> 20

<212> DNA

<213> Corynebacterium glutamicum

<400> 11
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tggtcgtggt  cttaccagca                                                          20
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<210> 12

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223>   Synthetic DNA

<400>   12
gatctagagg ttgccggtaa tcctgttg   28

<210>   13

<211>   28

<212>   DNA

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<220>

<223>   Synthetic DNA

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gatctagacg caggctgcca gcttattc   28

<210>   14

<211>   20

<212>   DNA

<213>   Corynebacterium glutamicum

<400>   14
atgaggttgt ccgtgacatg   20